contaminants. When considering ethical animal production practices, consideration needs to be given to the system impacts. In most situations, welfare-friendly production requires more land units per animal or per unit of product. Consideration of energy inputs into the system may be needed as energy use profoundly affects the ecological footprint left by an operation.

Key Words: Environment, Welfare, Organic

Breeding and Genetics - Livestock and Poultry: Poultry

40 Genetic variations in chicken aggressive behavior: the role of serotonergic system. R. L. Dennis*[1,2], Z. Q. Chen[3], and H. W. Cheng[1], [1]*Livestock Behavior Research Unit, USDA-ARS*, *West Lafayette, IN*, [2]*Purdue University*, *West Lafayette, IN*, [3]*Zheijiang University, School of Animal Science*, *Hangzhou, Zhejiang Province, China*.

Serotonin (5-HT) regulates aggressive behavior via binding to its receptors, such as 5HT-1A and -1B, in humans and rodents. This study was designed to test if 5-HT regulating aggressiveness has a heritable component in chickens. Chickens from two divergently selected lines KGB and MBB (low and high aggressiveness, respectively) and DXL (Dekalb XL, an aggressive out-group) were used in the study. Hens were paired within the same strain. At 24 wk of age, the subordinate of each pair received i.p. injection of either NAN-190 (1mg/kg, a 5HT-1A antagonist, NAN), GR-127935 (1mg/kg, a 5HT-1B antagonist, GR) or saline (control) for 5 days (n= 10 per strain). Frequency of aggressive behaviors were increased in the hens of DXL and MBB treated with NAN ($P<0.05$) and in the KGB hens treated with GR ($P<0.05$), respectively. GR treated KGB hens ($P<0.05$) and NAN treated MBB hens ($P<0.05$) also displayed an increased feather pecking (FP); but neither antagonist had an effect on FP of DXL hens ($P>0.05$). This may suggest the possibility of multiple mediating factors altering FP behaviors. Among the controls, MBB hens have higher epinephrine (EP) levels than KGB or DXL hens, indicative of the inferior stress coping ability of MBB hens. Treatment with GR significantly reduced EP levels in MBB hens ($P<0.05$), but not in DXL or KGB hens, suggesting a role of 5HT-1B in stress regulation in MBB hens. Hens of all strains treated with GR but not NAN exhibited reduced weight gain and increased plasma 5-HT concentrations compared to controls ($P<0.05$), suggesting a negative feedback system altering stress coping ability. The results provide evidence for different heritable serotonergic mediation of stress coping, aggression, and FP behaviors in chickens with high and low aggressive propensities. The data also indicates that, similar to humans and rodents, 5-HT-1A and -1B have different functions in the regulation of aggressive behaviors in chickens.

Key Words: Serotonin, Aggression, Hen

41 Association between SNPs and mortality in commercial broilers: a machine learning approach. N. Long*[1], D. Gianola[1], K. A. Weigel[1], G. J. M. Rosa[1], and S. Avendaño[2], [1]*University of Wisconsin*, *Madison*, [2]*Aviagen Ltd.*, *Newbridge, Scotland*.

Genome-wide association studies using single nucleotide polymorphisms (SNPs) can identify genetic variants related to complex traits. An objective is to find sets of relevant SNPs, and to combine them in a model that predicts phenotypes of individuals or groups. Typically, there are thousands of SNPs genotyped, but the number of phenotypes is smaller. An efficient method of selecting influential SNP markers is required; subsequently, more elaborate statistical modeling work can be conducted. A 2-step feature selection method for binary traits was developed, which consisted of filtering (using information gain), and wrapping (using naïve Bayesian classification). The filter reduces the large number of SNPs to a much smaller size, to facilitate the wrapper step. Also, an approach based on discretization for dealing with continuous phenotypic values in a classification framework was developed, to enable feature selection. The methods were applied to chick mortality rates on progeny from 201 sires in a commercial broiler, with the goal of identifying SNPs (over 5000) related to progeny mortality. To mimic a case-control study, sires were clustered into two groups, low and high, according to two arbitrarily chosen mortality cut points. By varying these thresholds, 11 different "case-control" samples were formed, and the 2-step feature selection procedure was applied to each. To compare the 11 sets of chosen SNPs, an ANOVA was carried out, and p-value of overall model fit and the predicted residual sum of squares (PRESS) were used as end-points. The 2-step method improved greatly the naïve Bayesian classification accuracy over the case without feature selection (from around 50% to above 90% without and with feature selection in each case-control sample). There was consistency over the 11 case-control samples between the patterns of selected SNPs and the mutual information. The best case-control group (63 sires over or below the thresholds) had a small p-value (< 0.0001) and a relatively small PRESS value (0.59). The 17 SNPs selected using this group accounted for 36% of the variation in mortality rates across all sire groups.

Key Words: SNP-mortality Association, Machine Learning

42 Non-major histocompatibility complex effects on the outcome of Rous sarcoma virus in Arkansas Progressor and Regressor chicken lines. M. Spanakos*[1], S. M. Sullivan[1], L. K. Stamps[1], R. Kopulos[2], J. Thompson[1], G. F. Erf[1], and N. B. Anthony[1], [1]*University of Arkansas*, *Fayetteville*, [2]*Northern Illinois University*, *DeKalb, IL*.

The *B* complex, or the major histocompatibility complex (MHC) in chickens, has a direct effect on the development of Rous sarcoma virus (RSV)-induced tumors. Certain erythrocyte (*Ea*) alloantigen systems have also been shown to influence the regression of RSV-induced tumors. The objective of this study was to determine the effects of the *Ea-A* and *Ea-I* systems on the development of RSV-induced tumors within and between the Arkansas Progressor (AP) and Regressor (AR) chicken lines. The interactions between the *Ea-A* and *Ea-I* loci and the *B* complex were also examined. The AP line (B^{13}) has two segregating alleles at the *Ea-A* (A^4 and A^5) and *Ea-I* (I^2 and I^8) loci, while the AR line (B^{13} and B^{221}) is fixed at the *A* locus (A^4). Tumors were scored three times a week for a 10-week period. Pattern of response to the tumor was evaluated using tumor score (TS), tumor profile index (TPI), and mortality. Birds with the AP B^{13}, AR B^{13}, and AP B^{13}/AR B^{13} backgrounds and I^2I^8 haplotype had higher TS, TPI and mortality compared to those with the homozygous *Ea-I* combinations. A similar effect was seen with the *Ea-A* heterozygotes as compared to homozygotes in the AP B^{13}, and AP B^{13}/AR B^{13} backgrounds. Tumor

regression efficiency declined even further when an individual was heterozygous at both the *Ea-A* and *Ea-I* loci in the AP B^{13}, and AP B^{13}/AR B^{13} backgrounds. The observed decline in the efficiency of tumor regression as heterozygosity at the *Ea-A* and *Ea-I* loci increased suggests a dosage effect of the *Ea-A* and *Ea-I* systems. However the effects of the *Ea-A* and *Ea-I* loci seemed to be suppressed when the B^{221} allele was present. This suggests that the *B* locus has an epistatic effect on the *Ea-A* and *Ea-I* systems. Hence, in the AP and AR lines the effects of the *Ea-A* and *Ea-I* loci on the response to RSV challenge are expressed in the presence of the B^{13} allele.

Key Words: MHC, Erythrocyte Alloantigen Systems, Rous Sarcoma Tumor

43 Animal model estimation of (Co) variance components and genetic parameters for most important economic traits in Iranian native fowl. A. Ghazi Khani Shad*[1], A. Nejati Javaremi[2], and H. Mehrabani Yeganeh[2], [1]*Azad University of Science and Research*, *Tehran, Iran*, [2]*University of Tehran*, *Iran*.

(Co)Variance components and genetic parameters for economic traits in Iranian native fowls were estimated using multivariate animal model analysis with DFREML procedure. The data of four stations of native fowls breeding (Mazandaran:n= 49536, Esfahan:n= 23108, West Azarbaijan:n= 24890 and Fars: n=30279) was containing records of cocks and hens collected during period of 1988 to 2006. The recorded traits were body weight (at 8 weeks or 12 weeks), ge at first egg, egg number at 12 first weeks of production and mean egg weight between 28 to 32 weeks. The most estimated heritabilites, except egg number, were more than 0.20. The highest heritabilites for all traits were related to Fars station, whereas most heritabilites in West Azarbaijan were less than other stations. The heritability for egg number was estimated 0.099 ± 0.018 for Esfahan to 0.322±0.012 for Fars. The estimated heritabilities of body weight were medium to high and varied from 0.228 ± 0.014 for Esfahan to 0.548 ± 0.014 for Fars, While, the heritabilities of mean egg weight were high and ranged from 0.223 ± 0.021 for West Azarbaijan to 0.638 ± 0.013 for Fars. The heritability for Age at first egg was estimated 0.270 ± 0.021 for Esfahan to 0.520 ± 0.014 for Fars. The most estimated genetic correlations, except between Body weight and Egg weight and between age at first egg and egg weight, were negative.The direct genetic correlations between maturity age and egg number were high and negative, ranging from -0.384 ± 0.033 to -0.987 ± 0.003 for Mazandaran and Fars, respectively.

The estimated Heritabilites ± standard errors for BW, AFE, EN12 and MEW

	Mazandaran	Fars	West Azarbaijan	Esfahan
BW	0.279±0.009	0.548±0.014	0.254±0.014	0.228±0.014
AFE	0.346±0.012	0.520±0.014	0.276±0.027	0.270±0.021
EN12	0.158±0.009	0.322±0.012	0.099±0.018	0.185±0.019
MEW	0.458±0.012	0.638±0.014	0.223±0.021	0.246±0.022

BW, AFE,EN12 and MEW are body weight, age at first egg,egg number and mean egg weight, respectively

Key Words: Economic Traits, Heritability, Genetic Correlation

44 Effects of competition on expected response to selection for ADG. C. Y. Chen*[1], R. K. Johnson[1], S. D. Kachman[1], and L. D. Van Vleck[1,2], [1]*University of Nebraska*, *Lincoln*, [2]*ARS, USDA, U.S. Meat Animal Research Center*, *Clay Center, NE*.

The objective was to investigate the importance of competition effects on expected response to selection for average daily gain (ADG, g) of boars. A total of 9,720 records from dam lines (1 and 2) and sire lines (3 and 4) were available with 15 boars per pen. Gains (ADG) were measured from about 71 to 161 d of age and weight from 31 to 120 kg. Four models for EBV were compared; each included initial age on test as a covariate and fixed effect of contemporary group (farm-year-season). Direct genetic (d) and competition genetic (c) effects were included in models as random effects. Pen (pn) was included in some models as fixed and in other models as random factors. Models were: Model 1 (d, c, pn random) as full model, Model 2 (d and c), Model 3 (d and pn random), and Model 4 (d, pn fixed). Estimates of direct heritability with Model 1 obtained with MTDFREML for ADG were 0.31, 0.39, 0.21, and 0.26 for lines 1-4. Estimates of heritability of competition effects were near zero. Model 2 produced slightly larger estimates of competition variances ($P<0.05$ for lines 1-3). Expected responses to selection were calculated under the assumption that estimates of parameters from Model 1 were unbiased. For response of one genetic SD for both components (d and c), the proportions of expected total gain due to competition effects (with economic weights of 1 for each with pen size of 14) were 53, 19, 62, and 58% for the 4 lines. Rank correlations within lines were: 0.87-0.95, 0.51-0.99, and 0.36-0.97 between Model 1 and Models 2, 3, and 4. Genetic gains were calculated with pigs ranked on reduced models, but with EBV calculated with the best model (Model 1). Average total breeding values ($TEBV=EBV_d +14EBV_c$) for the top 10% of boars selected with Model 1 were 83, 110, 42, and 102 g for lines 1 to 4, respectively. For rankings based on Model 3, but EBV calculated with Model 1, average TEBV for the top 10% were 76, 110, 18, and 95 g and for rankings based on Model 4 were 66, 108, 12, and 87 g. Further study of correlated responses with models including competition effects seems warranted.

Key Words: Competition, Response to Selection, Swine

45 Effect of sex and sire on the intramuscular fatty acid profile in pigs. S. De Smet*[1], M. Ntawubizi[1], K. Raes[1,3], and N. Buys[2], [1]*Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Production, Ghent University*, *Melle, Belgium*, [2]*Centre for Animal Genetics and Selection, Catholic University Leuven*, *Heverlee, Belgium*, [3]*University College of West-Flanders, Department PIH*, *Kortrijk, Belgium*.

Intramuscular (IM) fatty acid (FA) composition is affected by dietary and genetic factors. The aim of this study was to investigate the effect of sex and sire on the IM FA profile of pork. Indices reflecting activities of desaturase and elongase enzymes involved in FA metabolism were calculated as ratio's of product to precursor FA proportions. The *Longissimus dorsi* from 123 animals (n = 61 castrates and 62 females) originating from 5 boars (n = 24-26 per boar) was analysed for FA composition. Pigs were all fattened on the same diet, and were slaughtered at a live weight of approximately 110 kg. The results of the FA proportions (g/100g FAME) were analysed using a General Linear Model with sex and sire as fixed effects (sex x sire interaction term not significant), and IM fat content as covariate to account for variation in the FA proportions due to differences in fatness. The IM fat

content had a highly significant effect on all individual polyunsaturated FA (PUFA) proportions, except C18:3n-3. The sum of n-6 and n-3 PUFA proportions were higher in females compared to castrates ($P<0.05$). Sire had no effect on the sum of n-6 PUFA, but affected the sum of n-3 PUFA ($P<0.001$). An effect of sire ($P<0.05$) but not of sex was observed for several indices reflecting de('Δ');9-desaturase activity. A significant ($P<0.001$) effect of sire was observed for most indices reflecting desaturase and elongase activities involved in the n-3 PUFA metabolism. A moderate effect of sex was found, with a higher capacity of females compared to castrates to elongate and desaturate C18:3n-3 to longer chain FA. The effects of sex and sire on the indices calculated within the n-6 PUFA series were less marked. The data suggest considerable genetic variability for the long chain PUFA metabolism independent of the level of fatness.

Key Words: Polyunsaturated Fatty Acids, Elongase/Desaturase Activity, Pig Muscle

46 Assessing hepatic gene expression in response to xenobiotic exposure. S. Boorgula*, D. J. Blodgett, M. Carlidge, S. Blevins, J. Boothe, and R. M. Lewis, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Xenobiotics from plant derived foreign chemicals are metabolized in liver when ingested. Phase I liver enzymes may change non-polar xenobiotics into reactive metabolites, thereby increasing toxicity. Phase II enzymes help inactivate these metabolites by addition of water-soluble groups and by their excretion in urine or bile. Some genes affecting expression of phase I enzymes are cytochrome P450 (Cyp) 1a2 and flavin mono-oxygenase (FMO) 1; and phase II enzymes are glutathione-S-transferase mu (Gstm) 1 and quinone reductase (Nq) 02. Xenobiotics of interest are ergotamine (ET), associated with fescue toxicosis, and sulforaphane (SFN), considered a phase II enzyme inducer. Although effects of SFN on phase I genes are unclear, ET is generally metabolized by phase I enzymes. Our objective was to test whether predicted variation in liver enzyme activity and gene expression occurred with exposure to these xenobiotics. Polymorphic mice (ICR, Harlan Sprague Dawley) were orally dosed for 2, 5, 8 or 11 d with either SFN (2.5 mg•mouse^{-1}•d^{-1}) or ET (0.6 mg•mouse^{-1}•d^{-1}) or control ($n \geq 5$ for each period and treatment). Control was a 50:50 mix of dimethyl sulfoxide and water, a vehicle used for diluting SFN and ET. Mice were killed 24h after last dosing and livers collected. Real time PCR revealed increase in expression ($P \leq 0.05$) of Cyp1a2 in both treatments relative to control on d 5, while FMO1 expression increased ($P \leq 0.05$) on d 11 in only SFN treated mice. Increase ($P < 0.05$) in expression of transcription factor, Nuclear factor-erythroid 2 p45-related factor 2 (Nrf2) and Nq02 ($P < 0.05$) gene on d 5 was followed by increase in Gstm1 expression ($P < 0.05$) on 8 and 11 d in SFN treated mice. Activity of Nq enzyme was decreased ($P < 0.05$) on d 8 in ET treated mice. Although, the down stream metabolism of FMO1 is not well documented, previous studies showed that Cyp1a2 inducers are deactivated in the presence of Gstm1. Thus, polymorphic mice, showing similarity in phase I gene (Cyp1a2) expression, but disparity in phase II gene (Gstm1 and Nq02) induction and enzyme activity, exhibited variable liver enzyme expression when challenged with different xenobiotics.

Key Words: Xenobiotics, Phase I and II Enzymes, Real Time PCR

47 Characterization of newly developed chicken 44K Agilent microarray. X. Y. Li*, H. I. Chiang, J. Zhu, and H. Zhou, *Texas A&M University*, *College Station*.

The development of high quality, reliable microarray resources for the chicken scientific community is an important step for avian functional genomics study. A new chicken 44K 60-mer oligonucleotide microarray featuring entire Marek's disease virus, avian influenza virus genomes, 150 chicken microRNAs and all gene models for the chicken genome has been developed on the Agilent platform. This new array provided a platform with four independent 44K arrays per slide. To characterize this array, four major tissues: liver, spleen, cecal tonsil, and ileum were collected from 6 commercial broilers and total RNA was isolated for hybridization to the microarray. A loop design was used to compare between every two tissues with dye swap and there were four biological replicates for each comparison. In total, 24 arrays were used in the current study. The signal intensity of each gene was normalized using LOWESS implemented in the R programming environment. More than 95% of spots had high signal to noise ratio (more than 10). A mixed model including fixed effects for tissue and dye was used to identify differentially expressed genes. There were 3710, 3355, 3208, 2886, 2660, and 358 genes significantly differentially expressed between spleen and ileum, liver and ileum, liver and cecal tonsil, liver and spleen, spleen and cecal tonsil, as well as cecal tonsil and ileum ($P<10^{-7}$) with corresponding false discovery rate (FDR) of 4.46×10^{-7}, 4.14×10^{-7}, 4.37×10^{-7}, 5.02×10^{-7}, 7.39×10^{-7} and 9.11×10^{-6}, respectively. Three to four hundred differentially expressed genes were more than 10-fold different for each comparison, except between cecal tonsil and ileum (18 genes). There existed 560, 108, 96, and 71 genes specifically expressed in liver, spleen, cecal tonsil, and ileum, respectively ($P<10^{-7}$). The results showed that this newly developed chicken oligonucleotide array is very informative and tissue-specific. This powerful genomic tool will provide a solid foundation for the further investigation in the areas of immunology, genetics, nutrition, and food safety in chickens.

Key Words: Chicken, Microarray, Functional Genome

48 Sources of variation in meat and carcass quality of pigs. E. F. Knol*, K. A. Engelsma, and J. W. M. Merks, *Institute for Pig Genetics (IPG)*, *Beuningen, The Netherlands*.

Predictable uniform pork quality is the goal for slaughter plants. 2526 animals of six sire lines and four dam crosses were born and raised on a Western European commercial farm and slaughtered and dissected in a large commercial slaughter plant to represent a standard situation. Phenotypic variation in 16 meat and 2 carcass quality traits was analyzed with ASReml and attributed to day of slaughter, weight, feeding system, sex, sire line, dam cross, litter and individual genetic variation. Heritabilities in strict sense were in line with literature values. Ratio between influence of sire line*dam cross and influence of slaughter day differed between 0.3 (Japanese color scale (JCS)) and 3.0 (drip loss) for meat quality. Recorded traits (h^2 ±SE) were: JCS loin (0.20 ±0.05), JCS inner ham (0.12 ±0.05), JCS outer ham (0.22 ±0.06), Minolta L (0.37 ±0.06), Minolta a (0.34 ±0.06), Minolta b (0.25 ±0.06), pH loin (0.23 ±0.05), pH ham (0.17 ±0.05), IMF (0.54 ±0.17), marbling loin (0.24 ±0.05), marbling ham (0.10 ±0.04), drip weight (0.23 ±0.06), drip score (0.15 ±0.05), drip loss (0.17 ±0.05), purge (0.18 ±0.06) and conductivity (0.27 ±0.06). For the two most relevant carcass traits (h^2 ±SE): deboned loin weight (0.28 ±0.06) and deboned ham weight (0.36 ±0.06). Genetic correlations between meat

quality traits show opportunities for indirect measurements (Minolta, pH and conductivity), they also show possibilities for simplified measurements (drip score). Heritabilities are interestingly high. Repeated meat quality measurements will further decrease the error term and increase the effective heritability. Uniformity in meat quality can be improved by using uniform sire line*dam cross, standardized shipping and processing, and genetic selection.

Key Words: Meat Quality, Variation, Heritability

49 Using a web-based economic model to examine investment decisions in the turkey industry for both integrated and non-integrated companies. B. J. Wood* and N. Buddiger, *Hybrid Turkeys*, *Kitchener, Ontario, Canada*.

An economic model for both integrated and non-integrated turkey production companies was created for use as a web-based management tool. Modeling turkey production was possible as all variables, from the supply of parent stock (PS) through to carcass processing and sale of final product, were readily quantified. Costs of production included PS and hatching costs related to poult production, feed, housing and labor for both the poult and commercial live production and finally manufacturing costs in the processing plant. Returns were generated though the sale of processed final product. At each level manipulation of PS strain, feed, labor, housing and processing had an effect on profitability and to accurately access the impact of each, the model should reflect the change in profitability of the system when production parameters were altered. Parameters higher in the production chain such as commercial poult cost and PS selection affected lower elements in the model such as the live production cost which ultimately affects the gross margin. Price volatility in feed and breast meat price were modeled with Gompertz-type growth and feed intake equations. This allowed optimal slaughter age or weight windows to be calculated based on feed price and processed product value. As feed price decreased or processed breast meat price increased the optimal slaughter weight also increased, conversely, with increased feed or lower breast meat price, the opposite was true, with a decrease in the optimal slaughter weight because of lower feed efficiencies at later ages. In each case, a decision on investment in feed and facilities must be made. Economic modeling can increase profitability via the ability to identify areas in which changes in management or investment can be made to improve performance. By examining the profit to investment ratio, investment may be made in an economically rational manner with funds channeled to areas that best increase the profit to investment ratio.

Key Words: Economic Model, Turkeys, World Wide Web

50 Quantitative and biological issues of feed utilization efficiency. S. E. Aggrey*, *University of Georgia*, *Athens*.

Most parametric statistical tests assume an additive rather than proportional error model. Since FC and BWG do not have similar distributions, the ratios of the two tend to be asymmetric (skewed). This violates the normality assumption the normality assumption of most statistical tests. The central limit theorem affords little protection for most skewed distributions, and when the sample size is small, the P-values associated with parametric tests like the t-test and ANOVA is incorrect. Summary statistics of FCR and FE yield different quantities. Log (any base) transformation of FE and FCR has the advantage of transforming the error model from a proportional to an additive one because log (FC/BWG)=log (FC) – log (BWG). Distributions of log values and consequently log ratios tends to be normal. Summary statistics of log ratios yield the same quantities, regardless of numerator/denominator assignments. The difference in sign of the means reflects whether on average the numerator is larger [+] or smaller [-] than the denominator. Taking the antilog of the average log ratios returns the data to a fold-metric.

Key Words: Feed Conversion Ratio, Feed Efficiency, Log Transformation

Egg and Meat Science and Muscle Biology - Livestock and Poultry: Meat Packaging and Shelf Life

51 Overview of meat life cycle from harvest to consumer. R. D. Huffman*[1] and J. C. Brooks[2], [1]*American Meat Institute Foundation*, *Washington, DC*, [2]*Texas Tech University*, *Lubbock*.

The harvest, processing and distribution of perishable meat products presents myriad challenges with respect to maintaining optimum quality and safety attributes. Frequently, the marketing term ″fresh″ is used to describe desirable product attributes and conversely, the term ″spoiled″ may be used to describe product that is no longer desirable for consumption. Product safety however is an attribute that should be decoupled from these product quality descriptors. When livestock are harvested, there exists an intrinsic potential for shelf life of the products derived from the carcass. The meat processing sector has developed numerous innovative means of protecting the integrity of raw meat products and maximizing potential shelf life of each product type. The processing steps and appropriate application of technology will determine how closely potential shelf life is maximized. This paper will describe the life cycle of meat products from the point of slaughter to the point of consumption, and attempt to clarify the meaning of the terms “fresh” and “spoiled.” The history of meat preservation dates back centuries and involves such important innovations as the first uses of salt in ancient times and the advent of mechanical refrigeration in the 1930’s. No doubt, these innovations were critical to the evolution of meat preservation; however, the most important recent innovation for increasing raw product shelf life is widespread adoption of vacuum packaging. Recent innovations have enabled the processing sector to further maximize fresh shelf life. Three major factors contribute to raw meat deterioration, 1) microbiological growth, 2) oxidation of lipids and 3) enzymatic activity. These factors are not mutually exclusive and in fact may interact to ultimately determine the end of shelf life. Optimum refrigeration at critical points in the harvest process, time and temperature controls throughout processing and distribution, reduction or elimination of oxygen exposure through packaging, and reduction of UV light exposure are all control methods that will mitigate the three factors that lead to product deterioration.

Key Words: Meat, Packaging, Shelf Life